Database :

UniProt_02:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		र्ह				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
, 						
1	1328	99.6	349	1	GUB_FIBSU	P17989 fibrobacter
2	266.5	20.0	259	1	GUB_BACBR	P37073 bacillus br
3	266.5	20.0	851	2	Q9K7X5	Q9k7x5 bacillus ha
4	248.5	18.6	256	2	Q9APD8	Q9apd8 bacillus ci
5	247.5	18.6	276	2	Q45648	Q45648 bacillus sp
6	245.5	18.4	214	2	Q8GMY0	Q8gmy0 bacillus li
7	245.5	18.4	242	1	GUB_BACSU	P04957 bacillus su
8	244.5	18.3	215	2	Q84GK1	Q84gk1 bacillus li
9	243	18.2	334	2	Q84C00	Q84c00 clostridium
10	242.5	18.2	214	2	Q93GE8	Q93ge8 uncultured
11	242.5	18.2	802	1	XYND RUMFL	Q53317 ruminococcu
12	242.5	18.2	802	2	Q9S310	Q9s310 ruminococcu
13	241.5	18.1	214	2	Q93GE7	Q93ge7 uncultured
						-

Database : PIR_79:*

1: pir1:* 2: pir2:* 3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ક			١	
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	1328	99.6	349	2	A44507	licheninase (EC 3.
2	266.5	20.0	851	2	H84053	endo-beta-1,3-1,4
3	265.5	19.9	252	2	A48378	licheninase (EC 3.
4	247.5	18.6	276	2	, I40453	licheninase (EC 3.
5	245.5	18.4	242	1	LXBS	licheninase (EC 3.
6	242.5	18.2	802	2	A36910	xylanase, beta(1,3
7	238.5	17.9	239	1	A29091	licheninase (EC 3.
8	237	17.8	334	1	S23498	licheninase (EC 3.
9	229.5	17.2	243	1	S15388	licheninase (EC 3.
10	226	17.0	237	1	S11927	licheninase (EC 3.
11	225	16.9	238	1	S19012	licheninase (EC 3.

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		% Query				
No.	Score		Length	DB	ID	Description
1	1103	82.7	228	3	US-09-286-690-12	Sequence 12, Appl
2	257.5	19.3	308	4	US-09-463-862A-1	Sequence 1, Appli
3	245.5	18.4	242	3	US-09-286-690-8	Sequence 8, Appli
4	244	18.3	239	1	US-08-103-998-2	Sequence 2, Appli
5	231.5	17.4	279	3	US-09-286-690-9	Sequence 9, Appli
6	229.5	17.2	243	3	US-09-286-690-10	Sequence 10, Appl
7	225	16.9	238	3	US-09-286-690-7	Sequence 7, Appli
8	222.5	16.7	242	3	US-09-286-690-11	Sequence 11, Appl
9	220.5	16.5	237	1	US-08-103-998-4	Sequence 4, Appli
10	200.5	15.0	526	4	US-09-248-796A-14807	Sequence 14807, A
11	189	14.2	245	3	US-09-286-690-2	Sequence 2, Appli
12	185	13.9	462	4	US-09-248-796A-14808	Sequence 14808, A

Database : A_Geneseq_23Sep04:* 1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2002s:* 6: geneseqp2003as:* 7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Query				
Score	Match	Length	DB 	ID	Description
257.5	19.3	308	2	AAW93001	Aaw93001 B. alkalo
246.5	18.5	242	1	AAP95000	Aap95000 Bacillus
244	18.3	214	4	AAE07317	Aae07317 Barley re
244	18.3	239	2	AAR06621	Aar06621 Hybrid (1
230	17.3	212	5	ABP58995	Abp58995 Paenibaci
226	17.0	234	2	AAR03775	Aar03775 Thermosta
226	17.0	237	2	AAR05803	Aar05803 Heat-stab
225	16.9	208	5	ABB76858	Abb76858 Bacterial
225	16.9	214	5	ABB76859	Abb76859 Bacterial
220.5	16.5	237	2	AAR06622	Aar06622 Hybrid (1
204.5	15.3	504	8	ADP98858	Adp98858 C. albica
189	14.2	245	2	AAW37884	Aaw37884 Lichenase
185	13.9	453	7	ADC01836	Adc01836 C. albica
185	13.9	453	8	ADP98992	Adp98992 C. albica
	257.5 246.5 244 244 230 226 226 225 225 220.5 204.5 189 185	Query Score Match 257.5 19.3 246.5 18.5 244 18.3 244 18.3 230 17.3 226 17.0 226 17.0 225 16.9 225 16.9 220.5 16.5 204.5 15.3 189 14.2 185 13.9	Query Score Match Length 257.5 19.3 308 246.5 18.5 242 244 18.3 214 244 18.3 239 230 17.3 212 226 17.0 234 226 17.0 237 225 16.9 208 225 16.9 208 225 16.9 214 220.5 16.5 237 204.5 15.3 504 189 14.2 245 185 13.9 453	Query Score Match Length DB 257.5 19.3 308 2 246.5 18.5 242 1 244 18.3 214 4 244 18.3 239 2 230 17.3 212 5 226 17.0 234 2 226 17.0 237 2 225 16.9 208 5 225 16.9 208 5 225 16.9 214 5 220.5 16.5 237 2 204.5 15.3 504 8 189 14.2 245 2 185 13.9 453 7	Query Score Match Length DB ID 257.5 19.3 308 2 AAW93001 246.5 18.5 242 1 AAP95000 244 18.3 214 4 AAE07317 244 18.3 239 2 AAR06621 230 17.3 212 5 ABP58995 226 17.0 234 2 AAR03775 226 17.0 237 2 AAR05803 225 16.9 208 5 ABB76858 225 16.9 214 5 ABB76859 220.5 16.5 237 2 AAR06622 204.5 15.3 504 8 ADP98858 189 14.2 245 2 AAW37884 185 13.9 453 7 ADC01836

Database :

PIR_79:*

1: pir1:*

2: pir2:* 3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ફ				
	Query				
Score	Match	Length	DB	ID	Description
2020.5	70.5	720	2	T52564	Mrell protein homo
852.5	29.8	649	1	S58097	probable dna repai
768	26.8	692	1	S57592	probable phosphoes
724	25.3	772	2	T27512	hypothetical prote
178	6.2	443	1	G69378	probable phosphoes
175.5	6.1	423	2	E75103	phosphoesterase ho
174.5	6.1	413	1	D71083	probable phosphoes
163.5	5.7	587	1	E69171	phosphoesterase-re
150.5	5.3	381	2	C90395	DNA repair protein
143	5.0	1038	2	JC5497	claustrin - chicke
141.5	4.9	409	2	E72765	probable phosphoes
136	4.7	1957	2	T38077	hypothetical coile
	2020.5 852.5 768 724 178 175.5 174.5 163.5 150.5 143 141.5	Query Score Match 2020.5 70.5 852.5 29.8 768 26.8 724 25.3 178 6.2 175.5 6.1 174.5 6.1 163.5 5.7 150.5 5.3 143 5.0 141.5 4.9	Query Score Match Length 2020.5 70.5 720 852.5 29.8 649 768 26.8 692 724 25.3 772 178 6.2 443 175.5 6.1 423 174.5 6.1 413 163.5 5.7 587 150.5 5.3 381 143 5.0 1038 141.5 4.9 409	Query Score Match Length DB 2020.5 70.5 720 2 852.5 29.8 649 1 768 26.8 692 1 724 25.3 772 2 178 6.2 443 1 175.5 6.1 423 2 174.5 6.1 413 1 163.5 5.7 587 1 150.5 5.3 381 2 143 5.0 1038 2 141.5 4.9 409 2	Query Score Match Length DB ID 2020.5 70.5 720 2 T52564 852.5 29.8 649 1 S58097 768 26.8 692 1 S57592 724 25.3 772 2 T27512 178 6.2 443 1 G69378 175.5 6.1 423 2 E75103 174.5 6.1 413 1 D71083 163.5 5.7 587 1 E69171 150.5 5.3 381 2 C90395 143 5.0 1038 2 JC5497 141.5 4.9 409 2 E72765

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Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		र्ठ				
Result		Query	•			
No.	Score	Match	Length	DB	ID	Description
1	2864	100.0	552	4	US-09-835-654-2	Sequence 2, Appli
2	2020.5	70.5	720	3	US-09-480-921B-8	Sequence 8, Appli
3	954.5	33.3	680	4	US-09-538-092-1165	Sequence 1165, Ap
4	768	26.8	692	4	US-09-538-092-632	Sequence 632, App
5	507.5	17.7	270	4	US-09-248-796A-19151	Sequence 19151, A
6	141.5	4.9	132	4	US-09-270-767-33195	Sequence 33195, A
7	141.5	4.9	132	4	US-09-270-767-48412	Sequence 48412, A
8	136	4.7	857	4	US-09-248-796A-20522	Sequence 20522, A
9	122	4.3	1120	3	US-09-147-404-1	Sequence 1, Appli
10	122	4.3	1935	4	US-09-538-092-916	Sequence 916, App